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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,430

DATE: 12/17/2001

TIME: 11:07:09

Input Set : A:\RTS-0341 Sequence Listing.txt

Output Set: N:\CRF3\12172001\J006430.raw

ENTERED

4 <110> APPLICANT: Mark J. Graham
 5 Kenneth Dobie
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF CD81 EXPRESSION
 9 <130> FILE REFERENCE: RTS-0341
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/006,430
 C--> 11 <141> CURRENT FILING DATE: 2001-12-10
 11 <160> NUMBER OF SEQ ID NOS: 90
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 20
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 21 <223> OTHER INFORMATION: Antisense Oligonucleotide
 23 <400> SEQUENCE: 1 20
 24 tccgtcatcg ctccctcaggg
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 20
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 34 <223> OTHER INFORMATION: Antisense Oligonucleotide
 36 <400> SEQUENCE: 2 20
 37 atgcattctg cccccaagga
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 1496
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Homo sapiens
 45 <220> FEATURE:
 47 <221> NAME/KEY: CDS
 48 <222> LOCATION: (239)...(949)
 50 <400> SEQUENCE: 3
 51 ccattgtgct ggaaaggcgc gcaacggcgg cgacggcggc gacccaccg cgcattcctgc 60
 53 caggectccg cgcccagccg cccacgcgcc ccgcgcgcc gcgcccgcac cctttcttcg 120
 55 cgccccgcgc cctcggcccg ccaggccccc ttgcgcgcca ccgcccagge ccgcgcgcgg 180
 57 ccgcgcgcgc gccacaggacc ggcccgcgcc ccgcaggcgc cccgcgcgcc gcgcgcgc 238
 61 atg gga gtg gag ggc tgc acc aag tgc atc aag tac ctg ctc ttc gtc 286
 62 Met Gly Val Glu Gly Cys Thr Lys Cys Ile Lys Tyr Leu Leu Phe Val
 63 1 5 10 15
 65 ttc aat ttc gtc ttc tgg ctg gct gga ggc gtg atc ctg ggt gtg gcc 334
 66 Phe Asn Phe Val Phe Trp Leu Ala Gly Gly Val Ile Leu Gly Val Ala
 67 20 25 30
 69 ctg tgg ctc cgc cat gac ccg cag acc acc aac ctc ctg tat ctg gag 382
 70 Leu Trp Leu Arg His Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu
 71 35 40 45
 73 ctg gga gac aag ccc gcg ccc aac acc ttc tat gta ggc atc tac atc 430
 74 Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile
 75 50 55 60

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77 ctc atc gct gtg ggc act gtc atg atg ttc gtt ggc ttc ctg ggc tgc 478
78 Leu Ile Ala Val Gly Ala Val Met Met Phe Val Gly Phe Leu Gly Cys
79 65 70 75 80
81 tac ggg gcc atc cag gaa tcc cag tgc ctg ctg ggg acg ttc ttc acc 526
82 Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr
83 85 90 95
85 tgc ctg gtc atc ctg ttt gcc tgt gag gtg gcc gcc ggc atc tgg ggc 574
86 Cys Leu Val Ile Leu Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly
87 100 105 110
89 ttt gtc aac aag gac cag atc gcc aag gat gtg aag cag ttc tat gac 622
90 Phe Val Asn Lys Asp Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp
91 115 120 125
93 cag gcc cta cag cag gcc gtg gtg gat gat gac gcc aac aac gcc aag 670
94 Gln Ala Leu Gln Gln Ala Val Val Asp Asp Asp Ala Asn Asn Ala Lys
95 130 135 140
97 gct gtg gtg aag acc ttc cac gag acg ctt gac tgc tgt ggc tcc agc 718
98 Ala Val Val Lys Thr Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser
99 145 150 155 160
101 aca ctg act gct ttg acc acc tca gtg ctc aag aac aat ttg tgt ccc 766
102 Thr Leu Thr Ala Leu Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro
103 165 170 175
105 tcg ggc agc aac atc atc agc aac ctc ttc aag gag gac tgc cac cag 814
106 Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln
107 180 185 190
109 aag atc gat gac ctc ttc tcc ggg aag ctg tac ctc atc ggc att gct 862
110 Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala
111 195 200 205
113 gcc atc gtg gtc gct gtg atc atg atc ttc gag atg atc ctg agc atg 910
114 Ala Ile Val Val Ala Val Ile Met Ile Phe Glu Met Ile Leu Ser Met
115 210 215 220
117 gtg ctg tgc tgt ggc atc cgg aac agc tcc gtg tac tga ggccccgcag 959
118 Val Leu Cys Cys Gly Ile Arg Asn Ser Ser Val Tyr
119 225 230 235
121 ctctggccac agggacctct gcagtgcgcc ctaagtgacc cggacaacttc cgaggggggcc 1019
122 atcaccgcct gtgtatataa cgtttccggt attactctgc tacacgtagc ctttttactt 1079
123 ttgggggtttt gtttttgttc tgaactttcc tggtaccttt tcagggctga tgtcacatgt 1139
124 aggtggcggtg tatgagtgga gacgggcctg ggtcttgggg actggagggc aggggtcctt 1199
125 ctgccccctgg ggtcccaggg tgctctgcct gctcagccag gcctctcctg ggagccactc 1259
126 gccagagac tcagcttggc caacttgggg ggcgtgtgcc accagcccg cccgtcctgt 1319
127 gggctgcaca gctcaccttg ttccctcctg ccccggttcg agagccgagt ctgtgggcac 1379
128 tctctgcctt catgcacctg tcccttctaa cacgtcgct tcaactgtaa tcacaacatc 1439
129 ctgactccgt catttaataa agaaggaaca tcaggcatgc taaaaaaaa aaaaaaa 1496
140 <210> SEQ ID NO: 4
141 <211> LENGTH: 20
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
144 <214> FEATURE:
145 <215> OTHER INFORMATION: PCR Primer
146 <216> SEQUENCE: 4

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150 cagatcgcca aggatgtgaa 20
153 <210> SEQ ID NO: 5
154 <211> LENGTH: 18
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
160 <223> OTHER INFORMATION: PCR Primer
162 <400> SEQUENCE: 5
163 gcgttggttg cgtcatca 18
166 <210> SEQ ID NO: 6
167 <211> LENGTH: 28
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
173 <223> OTHER INFORMATION: PCR Probe
175 <400> SEQUENCE: 6
176 agttctatga ccaggcccta cagcaggc 28
179 <210> SEQ ID NO: 7
180 <211> LENGTH: 19
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
186 <223> OTHER INFORMATION: PCR Primer
188 <400> SEQUENCE: 7
189 aaaggtgaag gtcggagtc 19
192 <210> SEQ ID NO: 8
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
199 <223> OTHER INFORMATION: PCR Primer
201 <400> SEQUENCE: 8
202 gaagatggtg atgggatttc 20
205 <210> SEQ ID NO: 9
206 <211> LENGTH: 20
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
212 <223> OTHER INFORMATION: PCR Probe
214 <400> SEQUENCE: 9
215 caagcttccc gttctcagcc 20
218 <210> SEQ ID NO: 10
219 <211> LENGTH: 626
220 <212> TYPE: DNA
221 <213> ORGANISM: Homo sapiens
223 <220> FEATURE:
225 <400> SEQUENCE: 10
226 atccgagcct gtgcttgctg ggcacggaa cagctcgtgt attgagtcct gcagctttgg 60
228 ccacaagaac ttctgcagtg cccctaagt gacccggaca cttccgaggg gaccatcacc 120

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230 gectgtgtat ataacgtttc cggattact ctgtacacg tagcctttt acctttgggg 180
232 ttttgttttt gttecgaaact ttctgttac ctttcaggg ctgacgtcac atgtagggtg 240
234 cgttatgag tggagacggg cctgggtctt ggggactgga gggcaggggt ccttctgcc 300
236 tgggtccca ggggtctctg cctgtcacg caggcctctc ctgggagcca ctgccccaga 360
238 gactcagctt ggcacaactt gggggctgtg tccaccacg ccgcccgctc tgtgggctgc 420
240 acaactcacc ttgttccctc ctgcccgggt tcgagagccg agtctgtggg cactctctgc 480
242 ctctatgcac ctgtcctttc taacacgtcg ccttcaactg taatcacac atctgactc 540
244 ctctatttaa taaagaagga acatcaggca tgctaccagg cctgtgcagt caaaaaaaaa 600
246 aaaaaaaaaa aaaaaaaaaa aaaaaa 626
249 <210> SEQ ID NO: 11
250 <211> LENGTH: 21501
251 <212> TYPE: DNA
252 <213> ORGANISM: Homo sapiens
254 <220> FEATURE:
256 <221> NAME/KEY: exon
257 <222> LOCATION: (518)...(812)
258 <223> OTHER INFORMATION: exon 1
W--> 260 <221> NAME/KEY: exon:intron junction
261 <222> LOCATION: (812)...(813)
262 <223> OTHER INFORMATION: exon 1:intron 1
264 <221> NAME/KEY: intron
265 <222> LOCATION: (813)...(13608)
266 <223> OTHER INFORMATION: intron 1
W--> 268 <221> NAME/KEY: intron:exon junction
269 <222> LOCATION: (13608)...(13609)
270 <223> OTHER INFORMATION: intron 1:exon 2
272 <221> NAME/KEY: exon
273 <222> LOCATION: (13609)...(13723)
274 <223> OTHER INFORMATION: exon 2
W--> 276 <221> NAME/KEY: exon:intron junction
277 <222> LOCATION: (13723)...(13724)
278 <223> OTHER INFORMATION: exon 2:intron 2
280 <221> NAME/KEY: intron
281 <222> LOCATION: (13724)...(17291)
282 <223> OTHER INFORMATION: intron 2
W--> 284 <221> NAME/KEY: intron:exon junction
285 <222> LOCATION: (17291)...(17292)
286 <223> OTHER INFORMATION: intron 2:exon 3
288 <221> NAME/KEY: exon
289 <222> LOCATION: (17292)...(17389)
290 <223> OTHER INFORMATION: exon 3
W--> 292 <221> NAME/KEY: exon:intron junction
293 <222> LOCATION: (17389)...(17390)
294 <223> OTHER INFORMATION: exon 3:intron 3
296 <221> NAME/KEY: intron
297 <222> LOCATION: (17390)...(18168)
298 <223> OTHER INFORMATION: intron 3
W--> 300 <221> NAME/KEY: intron:exon junction
301 <222> LOCATION: (18168)...(18169)

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302 <223> OTHER INFORMATION: intron 3:exon 4
304 <221> NAME/KEY: exon
305 <222> LOCATION: (18169)...(18243)
306 <223> OTHER INFORMATION: exon 4
W--> 308 <221> NAME/KEY: exon:intron junction
309 <222> LOCATION: (18243)...(18244)
310 <223> OTHER INFORMATION: exon 4:intron 4
312 <221> NAME/KEY: intron
313 <222> LOCATION: (18244)...(18612)
314 <223> OTHER INFORMATION: intron 4
W--> 316 <221> NAME/KEY: intron:exon junction
317 <222> LOCATION: (18612)...(18613)
318 <223> OTHER INFORMATION: intron 4:exon 5
320 <221> NAME/KEY: exon
321 <222> LOCATION: (18613)...(18717)
322 <223> OTHER INFORMATION: exon 5
W--> 324 <221> NAME/KEY: exon:intron junction
325 <222> LOCATION: (18717)...(18718)
326 <223> OTHER INFORMATION: exon 5:intron 5
328 <221> NAME/KEY: intron
329 <222> LOCATION: (18718)...(19065)
330 <223> OTHER INFORMATION: intron 5
W--> 332 <221> NAME/KEY: intron:exon junction
333 <222> LOCATION: (19065)...(19066)
334 <223> OTHER INFORMATION: intron 5:exon 6
336 <221> NAME/KEY: exon
337 <222> LOCATION: (19066)...(19167)
338 <223> OTHER INFORMATION: exon 6
W--> 340 <221> NAME/KEY: exon:intron junction
341 <222> LOCATION: (19167)...(19168)
342 <223> OTHER INFORMATION: exon 6:intron 6
344 <221> NAME/KEY: intron
345 <222> LOCATION: (19168)...(19824)
346 <223> OTHER INFORMATION: intron 6
W--> 348 <221> NAME/KEY: intron:exon junction
349 <222> LOCATION: (19824)...(19825)
350 <223> OTHER INFORMATION: intron 6:exon 7
352 <221> NAME/KEY: exon
353 <222> LOCATION: (19825)...(19911)
354 <223> OTHER INFORMATION: exon 7
W--> 356 <221> NAME/KEY: exon:intron junction
357 <222> LOCATION: (19911)...(19912)
358 <223> OTHER INFORMATION: exon 7:intron 7
360 <221> NAME/KEY: intron
361 <222> LOCATION: (19912)...(20000)
362 <223> OTHER INFORMATION: intron 7
W--> 364 <221> NAME/KEY: intron:exon junction
365 <222> LOCATION: (20000)...(20001)
366 <223> OTHER INFORMATION: intron 7:exon 8

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:260 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:268 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:276 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:284 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:292 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:300 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:308 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:316 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:324 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:332 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:340 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:348 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:356 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:364 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11